

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 3, 2005, 22:36:25 ; Search time 46 Seconds

(Without alignments)  
539.189 Million cell updates/sec

Title: US-09-518-931-2

Perfect score: 1634

Sequence: 1 MRALEGPGSLLCLVLALPA.....RVARMPLGERSVRERFLPVH 300

Scoring table: BLOSUM62

Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0% ; Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgm2\_6/prodata/1/iaa/6 COMB .pep:\*

3: /cgm2\_6/prodata/1/iaa/R COMB .pep:\*

4: /cgm2\_6/prodata/1/iaa/PCUTS COMB .pep:\*

5: /cgm2\_6/prodata/1/iaa/RE COMB .pep:\*

6: /cgm2\_6/prodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	1 US-08-794-796-2	Sequence 2, Appli
2	1634	100.0	300	2 US-09-532-27A-2	Sequence 2, Appli
3	1634	100.0	300	2 US-09-523-33-52	Sequence 52, Appli
4	1634	100.0	300	2 US-09-596-06A-1	Sequence 1, Appli
5	1634	100.0	300	2 US-09-536-09-3	Sequence 3, Appli
6	1634	100.0	333	2 US-09-949-016-7678	Sequence 7678, Appli
7	1619.5	99.1	299	2 US-09-586-59-17	Sequence 17, Appli
8	1491	91.2	271	2 US-09-536-09-1	Sequence 1, Appli
9	1177	72.0	211	2 US-09-286-59-20	Sequence 20, Appli
10	855	52.3	146	2 US-09-523-33-59	Sequence 59, Appli
11	841	51.5	153	2 US-09-586-59-2	Sequence 2, Appli
12	465.5	28.5	326	2 US-10-332-88-71	Sequence 71, Appli
13	465.5	28.5	326	2 US-09-538-06A-71	Sequence 61, Appli
14	447	27.4	401	2 US-10-332-88-62	Sequence 62, Appli
15	447	27.4	401	2 US-09-538-06A-62	Sequence 62, Appli
16	445	27.2	272	2 US-10-332-88-75	Sequence 75, Appli
17	445	27.2	272	2 US-09-538-06A-75	Sequence 75, Appli
18	445	27.2	321	2 US-10-332-88-80	Sequence 80, Appli
19	445	27.2	321	2 US-09-538-06A-80	Sequence 80, Appli
20	445	27.2	327	2 US-10-332-88-72	Sequence 72, Appli
21	445	27.2	327	2 US-09-538-06A-72	Sequence 72, Appli
22	445	27.2	351	2 US-10-332-88-74	Sequence 74, Appli
23	445	27.2	351	2 US-09-538-06A-74	Sequence 74, Appli
24	445	27.2	393	2 US-10-332-88-79	Sequence 79, Appli
25	445	27.2	393	2 US-09-538-06A-79	Sequence 79, Appli
26	445	27.2	399	2 US-10-332-88-73	Sequence 73, Appli
27	445	27.2	399	2 US-09-538-06A-73	Sequence 73, Appli

## ALIGNMENTS

RESULT 1  
US-08-794-796-2  
Sequence 2, Application US/08794796  
Patent No. 5885800

GENERAL INFORMATION:

APPLICANT: Emery, John  
APPLICANT: Tan, KB  
APPLICANT: Truneh, Alem  
APPLICANT: Young, Peter  
TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
TITLE OF INVENTION: TR4  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
ZIP: 19406

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PARTSED FOR Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794,796  
FILING DATE: 04-FEB-1997  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Han, William T  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: GH500000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-570-5219  
TELEFAX: 610-270-4026  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-794-796-2

Query Match Score 1634; DB 1; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.8e-127;

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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:09:15 ; Search time 68 Seconds  
(without alignments)

1843.365 Million cell updates/sec

Title: US-09-518-931-2

Perfect score: 1634

Sequence: 1 MFALEGPGQLSLICLVLALPA. .... RWARMPGLERSYRFLPVH 3 00

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

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2: /cgn2\_6/\_podata/1/\_pubpaa/us08\_pubcomb.pep: \*  
3: /cgn2\_6/\_podata/1/\_pubpaa/us09\_pubcomb.pep: \*  
4: /cgn2\_6/\_podata/1/\_pubpaa/us10\_pubcomb.pep: \*  
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6: /cgn2\_6/\_podata/1/\_pubpaa/us11\_pubcomb.pep: \*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	3 US-09-936-036A-1	Sequence 1, Appli
2	1634	100.0	300	3 US-09-934-924-1	Sequence 1, Appli
3	1634	100.0	300	3 US-09-935-727-2	Sequence 2, Appli
4	1634	100.0	300	4 US-10-129-709-3	Sequence 3, Appli
5	1634	100.0	300	4 US-10-125-905-2	Sequence 2, Appli
6	1634	100.0	300	4 US-10-310-793-6	Sequence 6, Appli
7	1634	100.0	300	4 US-10-369-300-19	Sequence 19, Appli
8	1634	100.0	300	4 US-10-375-680-52	Sequence 52, Appli
9	1634	100.0	300	4 US-10-418-242-2	Sequence 2, Appli
10	1634	100.0	300	4 US-10-556-819-1	Sequence 1, Appli
11	1634	100.0	300	4 US-10-733-263-2	Sequence 2, Appli
12	1634	100.0	300	4 US-10-888-132-1	Sequence 1, Appli
13	1634	100.0	300	4 US-10-466-785-3	Sequence 3, Appli
14	1634	100.0	300	5 US-10-971-907-1	Sequence 1, Appli
15	1634	100.0	300	5 US-10-775-180-145	Sequence 145, Appli
16	1634	100.0	300	5 US-10-775-180-151	Sequence 151, Appli
17	1634	100.0	300	5 US-10-775-180-157	Sequence 157, Appli
18	1634	100.0	300	5 US-10-775-180-158	Sequence 158, Appli
19	1634	100.0	300	5 US-10-943-197-49	Sequence 4, Appli
20	1634	100.0	300	5 US-10-775-204-439	Sequence 439, Appli
21	1634	100.0	300	5 US-10-775-204-452	Sequence 452, Appli
22	1634	100.0	300	5 US-10-775-204-491	Sequence 491, Appli
23	1634	100.0	300	5 US-10-775-204-494	Sequence 494, Appli
24	1634	100.0	341	4 US-10-106-638-4514	Sequence 4514, Appli
25	1634	100.0	885	5 US-10-775-180-88	Sequence 88, Appli
26	1634	100.0	885	5 US-10-775-180-89	Sequence 89, Appli
27	1634	100.0	885	5 US-10-775-204-275	Sequence 275, Appli

## ALIGNMENTS

RESULT 1  
US-09-896-096A-1  
; Sequence 1, Application US/09896096A1  
; Patent No. US20030061559A1  
; GENERAL INFORMATION:  
; APPLICANT: ASHKENAZI, AVI J  
; APPLICANT: BOTSTEIN, DAVID  
; APPLICANT: DODGE, KELLY H.  
; APPLICANT: GURNEY, AUSTIN L.  
; APPLICANT: KIM, KYUNG JIN  
; APPLICANT: LAWRENCE, DAVID A.  
; APPLICANT: PITTI, ROBERT A.  
; APPLICANT: ROY, MARGRET A.  
; APPLICANT: TUMAS, DANIEL B.  
; APPLICANT: WOOD, WILLIAM J.  
; TITLE OF INVENTION: DCR3 polypeptide, A TNFR Homolog  
; FILE REFERENCE: P1134R2 REVISED  
; CURRENT APPLICATION NUMBER: US 09/896,096A  
; PRIOR APPLICATION NUMBER: US 60/059,288  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 18  
; SEQ ID NO: 1  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-896-096A-1

Query Match 100.0% ; Score 1634; DB 3; Length 300;  
Best Local Similarity 100.0% ; Pred. No. 1.7e-124;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRALEPGISLILCLVLALPAIPLPVAVRGAETPTPWRDAETGERLVAQCPGTFVQR 60  
Db 1 MRALEPGISLILCLVLALPAIPLPVAVRGAETPTPWRDAETGERLVAQCPGTFVQR 60  
Qy 61 PRRDRSPPTCGCPCPRHYQFWNYLERCRCNVLGEREERACHATHNRACRTGFF 120  
Db 61 PRRDRSPPTCGCPCPRHYQFWNYLERCRCNVLGEREERACHATHNRACRTGFF 120  
Qy 121 AHGFCLEHASCPCGPGAGVIAFGTPSNTQCPPTGTSASSQCPHRNCTPAGLA 180  
Db 121 AHGFCLEHASCPCGPGAGVIAFGTPSNTQCPPTGTSASSQCPHRNCTPAGLA 180  
Qy 181 LNPGSSSHDTLCTSTCGPPLSLTRVYGAERCRERAVTFDVAQFDQDISTKRLQLQALEAPE 240  
Db 181 LNPGSSSHDTLCTSTCGPPLSLTRVYGAERCRERAVTFDVAQFDQDISTKRLQLQALEAPE 240

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CM protein - protein search, using SW model

Run on: December 3, 2005, 22:36:25 ; Search time 46 Seconds (without alignments)

539.189 Million cell updates/sec

Title: US-09-518-931-2

Perfect score: 1634

Sequence: 1 MRALEGPGLSSLICLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSSUM62

Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:  
4: /cgn2\_6/ptodata/1/iaa/PCUTS\_COMB.pep:  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:  
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\*  
\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	ID	Description
1	1634	100.0	300	1	US-09-794-796-2		Sequence 2, Appli
2	1634	100.0	300	2	US-09-632-27A-2		Sequence 2, Appli
3	1634	100.0	300	2	US-09-523-323-52		Sequence 2, Appli
4	1634	100.0	300	2	US-09-896-096A-1		Sequence 1, Appli
5	1634	100.0	300	2	US-09-936-019-3		Sequence 3, Appli
6	1634	100.0	333	2	US-09-749-016-778		Sequence 6, Appli
7	1619.5	99.1	299	2	US-09-286-529-17		Sequence 17, Appli
8	149.5	91.2	271	2	US-09-936-019-1		Sequence 1, Appli
9	1177	72.0	211	2	US-09-286-529-20		Sequence 20, Appli
10	855	52.3	146	2	US-10-323-123-59		Sequence 59, Appli
11	841	51.5	153	2	US-09-286-529-2		Sequence 2, Appli
12	465.5	28.5	326	2	US-10-322-058-71		Sequence 71, Appli
13	465.5	28.5	326	2	US-09-338-063A-71		Sequence 71, Appli
14	447	27.4	401	2	US-10-322-058-62		Sequence 62, Appli
15	447	27.4	401	2	US-09-338-063A-52		Sequence 62, Appli
16	445	27.2	272	2	US-10-322-058-75		Sequence 75, Appli
17	445	27.2	272	2	US-09-338-063A-75		Sequence 75, Appli
18	445	27.2	321	2	US-10-322-058-80		Sequence 80, Appli
19	445	27.2	321	2	US-09-338-063A-80		Sequence 80, Appli
20	445	27.2	327	2	US-10-322-058-72		Sequence 72, Appli
21	445	27.2	327	2	US-09-338-063A-72		Sequence 72, Appli
22	445	27.2	351	2	US-10-322-058-74		Sequence 74, Appli
23	445	27.2	351	2	US-09-338-063A-74		Sequence 74, Appli
24	445	27.2	393	2	US-10-322-058-79		Sequence 79, Appli
25	445	27.2	393	2	US-09-338-063A-79		Sequence 79, Appli
26	445	27.2	399	2	US-10-322-058-73		Sequence 73, Appli
27	445	27.2	399	2	US-09-338-063A-73		Sequence 73, Appli

#### ALIGNMENTS

RESULT 1									
US-08-794-796-2		Sequence 2, Application US/08794796							
		; Patent No. 5883800							
		GENERAL INFORMATION:							
		; APPLICANT: Emery, John							
		; APPLICANT: Tan, KB							
		; APPLICANT: Trunich, Ale							
		; APPLICANT: Young, Peter							
		; TITLE OF INVENTION: Tumor Necrosis Related Receptor,							
		; TITLE OF INVENTION: TR4							
		; NUMBER OF SEQUENCES: 2							
		; CORRESPONDENCE ADDRESS:							
		; ADDRESS: SmithKline Beecham Corporation							
		; STREET: 109 Swedeland Road							
		; CITY: King of Prussia							
		; STATE: PA							
		; ZIP: 19406							
		COMPUTER READABLE FORM:							
		; MEDIUM TYPE: Diskette							
		; COMPUTER: IBM Compatible							
		; OPERATING SYSTEM: DOS							
		; SOFTWARE: FastSEQ for Windows Version 2.0							
		; CURRENT APPLICATION DATA:							
		; APPLICATION NUMBER: US/08/794,796							
		; FILING DATE: 04-FEB-1997							
		; CLASSIFICATION: 514							
		; PRIOR APPLICATION DATA:							
		; APPLICATION NUMBER:							
		; FILING DATE:							
		; ATTORNEY/AGENT INFORMATION:							
		; NAME: Han, William T							
		; REGISTRATION NUMBER: 34,344							
		; REFERENCE/DOCKET NUMBER: GH50000							
		; TELECOMMUNICATION INFORMATION:							
		; TELEPHONE: 610-270-5219							
		; TELEX: 610-270-4046							
		; INFORMATION FOR SEQ ID NO: 2:							
		; SEQUENCES CHARACTERISTICS:							
		; LENGTH: 300 amino acids							
		; TYPE: amino acid							
		; STRANDEDNESS: single							
		; TOPOLOGY: linear							
		; MOLECULE TYPE: protein							
		; US-08-794-796-2							
		Query Match Score 1634; DB 1; Length 300;							
		Pred. No. 7 8e-127;							